

AMENDMENTS TO THE SPECIFICATION

Please replace paragraph 2 on page 8 of the specification, beginning at line 17 and ending at line 31, with the following amended paragraph:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm known to those of skill in the art. An example of a mathematical algorithm for comparing two sequences is the algorithm of Karlin and Altschul Proc. Natl. Acad. Sci. USA (1990) 87: 2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-5877. The NBLAST and XBLAST programs of Altschul et al, J. Mol. Biol. (1990) 215: 403-410 have incorporated such an algorithm. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilised as described in Altschul et al, Nucleic Acids Res. (1997) 25: 3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilising BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e. g. , NBLAST) can be used. See www.ncbi.nlm.nih.gov www.ncbi.nlm.nih.gov.

Please replace paragraph 1 on page 16 of the specification, beginning at line 1 and ending at line 17, with the following amended paragraph:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm known to those of skill in the art. An example of a mathematical algorithm for comparing two sequences is the algorithm of Karlin and Altschul Proc. Natl. Acad. Sci. USA (1990) 87: 2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-5877. The NBLAST and XBLAST programs of Altschul et al, J. Mol. Biol. (1990) 215: 403-410 have incorporated such an algorithm. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilised as described in Altschul et al, Nucleic Acids Res. (1997) 25: 3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilising BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e. g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov> www.ncbi.nlm.nih.gov.

Please replace the drawing description for Figure 20 on page 37, with the following amended text, which has been marked up to show the removal of the embedded hyperlink, as shown:

FIGURE 20 shows the cDNA encoding the mRNA of murine major urinary protein 1 (Mupl), (Accession no. NM 031188),), available from www.ncbi.nlm.nih.gov/entrez www.ncbi.nlm.nih.gov/entrez, published Lucke et al Eur. J. Biochem. 266 (3), 1210-1218 (1999); Abbate, et al J. Biomol. NMR 15 (2), 187-188 (1999); Ferrari et al FEBS Lett. 401 (1), 73-77 (1997); Held, et al Mol. Cell. Biol. 7 (10), 3705-3712 (1987) ; Bennett et al J. Cell Biol. 105 (3), 1073-1085 (1987); Shahan et al Mol. Cell. Biol. 7 (5), 1938-1946 (1987); Clark et al EMBO J. 4 (12), 3167-3171 (1985); Clark, et al EMBO J. 4 (12), 3159-3165 (1985); Ghazal et al Proc. Nat'l. Acad. Sci. USA. 82 (12), 4182-4185 (1985); Kuhn et al Nucleic Acids Res. 12 (15), 6073-6090 (1984); Clark et al EMBO J. 3 (5), 1045-1052 (1984); Krauter et al J. Cell Biol. 94 (2), 414-417 (1982) ; coding sequence from residues 112.. 654.

Please replace the drawing description for Figure 22 on page 37, with the following amended text, which has been marked up to show the removal of the embedded hyperlink, as shown:

FIGURE 22 shows the cDNA sequence encoding the mRNA of rat alpha-2-u globulin (accession no. M27434)), available from www.ncbi.nlm.nih.gov/entrez www.ncbi.nlm.nih.gov/entrez, published by Roy et al J. Steroid Biochem. 27 (4-6), 1129-1134 (1987)

Applicants submit that no new matter has been added by any of the amendments shown above.